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RAW SEQUENCE LISTING

PATENT APPLICATION: US/08/783,734D

DATE: 02/12/2003

TIME: 11:15:26

Input Set : A:\EP.txt

Output Set: N:\CRF4\02112003\H783734D.raw

3 <110> APPLICANT: Friedman, Jeffrey M.
 4 Lee, Gwo-Hua
 5 Proenca, Ricardo
 6 Ioffe, Ella
 8 <120> TITLE OF INVENTION: DB, THE RECEPTOR FOR LEPTIN, NUCLEIC ACIDS ENCODING THE
 RECEPTOR, AND
 9 USES THEREOF
 11 <130> FILE REFERENCE: 600-1-162CP2
 13 <140> CURRENT APPLICATION NUMBER: US 08/783,734D
 14 <141> CURRENT FILING DATE: 1997-01-16
 16 <150> PRIOR APPLICATION NUMBER: US 08/599,974
 17 <151> PRIOR FILING DATE: 1996-02-14
 19 <150> PRIOR APPLICATION NUMBER: US 08/586,594
 20 <151> PRIOR FILING DATE: 1996-01-16
 22 <160> NUMBER OF SEQ ID NOS: 126
 24 <170> SOFTWARE: PatentIn version 3.1
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 2529
 28 <212> TYPE: DNA
 29 <213> ORGANISM: Mus musculus
 31 <400> SEQUENCE: 1

ENTERED

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34	ccatgccgga tcagcaccag ctgttagctc gtgcgaatt cggcacgagg ttgcgttggg	120
36	aatgagcaag gtcaaaaactg ctctgcactc acagacaaca ctgaaggaa gacactggct	180
38	tca tagtga aggcttcagt tttcgccag cttaggttaa actgggacat agagtgtcg	240
40	atgaaagggg acttgacatt attcatctgt catatggagc cattacctaa gaacccttc	300
42	aagaattatg actctaaggc ccatcttttata tatgatctgc ctgaagtcata agatgattcg	360
44	cctctgcccc cactgaaaga cagcttcag actgtccaat gcaactgcag tcttcgggaa	420
46	tgtgaatgtc atgtgccgt acccagagcc aaactcaact acgctcttc gatgtatttg	480
48	gaaatcacat ctgccggtgt gagtttcag tcacctctga tgtcaactgca gcccattgtt	540
50	gttgtgaaac ccgatccacc cttaggtttg catatggaa tgacagatga tggtaattta	600
52	aagatttctt gggacagcca aacaatggca ccatttccgc ttcaatata ggtgaaatat	660
54	ttagagaatt ctacaattgt aagagaggct gctgaaattt tctcagctac atctctgt	720
56	gtagacagtg tgcttcctgg atcttcataat gaggtccagg tgaggagcaa gagactggat	780
58	gttccaggag tctggagtga ctggagttca cctcaagtct ttaccacaca agatgttg	840
60	tatttccac ccaaaaattct gactagtgtt ggatcgaatg cttctttca ttgcataetac	900
62	aaaaacgaaa accagattat ctccctaaaaa cagatagttt ggtggaggaa tctagctgag	960
64	aaaatccctg agatacagta cagcattgtg agtgaccgag ttagcaaatg taccttctcc	1020
66	aacctgaaag ccaccagacc tcgaggaaat tttacctatg acgcagtgtt ctgctgcaat	1080
68	gagcaggcgt gccatcaccg ctatgctgaa ttatacgtga tcgatgtcaa tatcaatata	1140
70	tcatgtgaaa ctgacgggta cttactaaa atgacttgca gatggtcacc cagcacaatc	1200
72	caatcactag tggaaagcac tggcagctg aggtatcaca ggcgcagcct gtattgtcct	1260
74	gatagtccat ctattcatcc tacgtctgag cccaaaaact gcgttaca gagagacggc	1320
76	tttatgaat gtgtttcca gccaatctt ctattatctg gctataataat gtggatcagg	1380

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78	atcaaccatt	ctttaggttc	acttgactcg	ccaccaaacgt	gtgtccttcc	tgactccgta	1440
80	gtaaaaccac	tacctccatc	taacgtaaaa	gcagagatta	ctgtaaacac	tggattattg	1500
82	aaagtatctt	gggaaaagcc	agtcttccg	gagaataacc	ttcaattcca	gattcgatat	1560
84	ggcttaagtg	aaaaagaaaat	acaatggaaag	acacatgagg	tattcgatgc	aaagtcaaag	1620
86	tctgccagcc	tgctgggtc	agacctctgt	gcagctatg	tggccaggt	tcgctgccgg	1680
88	cggtgtggatg	gactaggata	ttggagtaat	tggacagtc	cagcctatac	gcttgtcatg	1740
90	gatgtaaaag	ttcctatgag	agggcctgaa	ttttggagaa	aatggatgg	ggacgttact	1800
92	aaaaaggaga	gaaatgtcac	cttgctttgg	aagccctga	cgaaaaatga	ctcactgtgt	1860
94	agtgtgagga	ggtacgtggt	gaagcatcg	actgcccaca	atgggacgtg	gtcagaagat	1920
96	gtgggaaatc	ggaccaatct	cactttcctg	tggacagaac	cagcgcacac	tgttacagtt	1980
98	ctggctgtca	attccctcgg	cgcttccctt	gtgaatttta	accttacctt	ctcatggccc	2040
100	atgagtaaaag	tgagtgctgt	ggagtcaactc	agtgcttac	ccctgagcag	cagctgtgtc	2100
102	atccttcctt	ggacactgtc	acctgatgtat	tatagtctgt	tatatctgtt	tattgaatgg	2160
104	aagatcctta	atgaagatga	tggaatgaag	tggcttagaa	ttccctcgaa	tgttaaaaag	2220
106	tttatatatcc	acgataaattt	tattcccatc	gagaaatatac	agtttagtct	ttacccagta	2280
108	tttatggaaag	gagttggaaa	accaaagata	attaatggtt	tcaccaaaga	tgctatcgac	2340
110	aagcagcaga	atgacgcagg	gctgtatgtc	attgtaccca	taattatttc	ctcttgcgtc	2400
112	ctactgctcg	gaacactgtt	aatttcacac	cagagaatga	aaaagttgtt	ttgggacgat	2460
114	gttccaaacc	ccaagaattt	ttcctggca	caaggactga	atttccaaaa	gagaacggac	2520
116	actctttga						2529

119 <210> SEQ ID NO: 2

120 <211> LENGTH: 842

121 <212> TYPE: PRT

122 <213> ORGANISM: Mus musculus

124 <220> FEATURE:

125 <221> NAME/KEY: MISC_FEATURE

126 <222> LOCATION: (29)..(29)

127 <223> OTHER INFORMATION: X can be any amino acid

130 <400> SEQUENCE: 2

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-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

133	1				5				10					15		
-----	---	--	--	--	---	--	--	--	----	--	--	--	--	----	--	--

W--> 136 Gln Ala Leu Ser Pro Cys Arg Ile Ser Thr Ser Leu Xaa Leu Val Pro

137				20				25				30				
-----	--	--	--	----	--	--	--	----	--	--	--	----	--	--	--	--

140	Asn	Ser	Ala	Arg	Gly	Cys	Phe	Gly	Asn	Glu	Gln	Gly	Gln	Asn	Cys	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

141				35				40				45				
-----	--	--	--	----	--	--	--	----	--	--	--	----	--	--	--	--

144	Ala	Leu	Thr	Asp	Asn	Thr	Glu	Gly	Lys	Thr	Leu	Ala	Ser	Val	Val	Lys
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

145				50				55			60					
-----	--	--	--	----	--	--	--	----	--	--	----	--	--	--	--	--

148	Ala	Ser	Val	Phe	Arg	Gln	Leu	Gly	Val	Asn	Trp	Asp	Ile	Glu	Cys	Trp
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

149	65				70				75			80				
-----	----	--	--	--	----	--	--	--	----	--	--	----	--	--	--	--

152	Met	Lys	Gly	Asp	Leu	Thr	Leu	Phe	Ile	Cys	His	Met	Glu	Pro	Leu	Pro
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

153				85				90				95				
-----	--	--	--	----	--	--	--	----	--	--	--	----	--	--	--	--

156	Lys	Asn	Pro	Phe	Lys	Asn	Tyr	Asp	Ser	Lys	Val	His	Leu	Leu	Tyr	Asp
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

157				100				105				110				
-----	--	--	--	-----	--	--	--	-----	--	--	--	-----	--	--	--	--

160	Leu	Pro	Glu	Val	Ile	Asp	Asp	Ser	Pro	Leu	Pro	Pro	Leu	Lys	Asp	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

161				115				120			125					
-----	--	--	--	-----	--	--	--	-----	--	--	-----	--	--	--	--	--

164	Phe	Gln	Thr	Val	Gln	Cys	Asn	Cys	Ser	Leu	Arg	Gly	Cys	Glu	Cys	His
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

165				130				135			140					
-----	--	--	--	-----	--	--	--	-----	--	--	-----	--	--	--	--	--

168	Val	Pro	Val	Pro	Arg	Ala	Lys	Leu	Asn	Tyr	Ala	Leu	Leu	Met	Tyr	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

169	145				150				155			160				
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Input Set : A:\EP.txt

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172 Glu Ile Thr Ser Ala Gly Val Ser Phe Gln Ser Pro Leu Met Ser Leu
173 165 170 175
176 Gln Pro Met Leu Val Val Lys Pro Asp Pro Pro Leu Gly Leu His Met
177 180 185 190
180 Glu Val Thr Asp Asp Gly Asn Leu Lys Ile Ser Trp Asp Ser Gln Thr
181 195 200 205
184 Met Ala Pro Phe Pro Leu Gln Tyr Gln Val Lys Tyr Leu Glu Asn Ser
185 210 215 220
188 Thr Ile Val Arg Glu Ala Ala Glu Ile Val Ser Ala Thr Ser Leu Leu
189 225 230 235 240
192 Val Asp Ser Val Leu Pro Gly Ser Ser Tyr Glu Val Gln Val Arg Ser
193 245 250 255
196 Lys Arg Leu Asp Gly Ser Gly Val Trp Ser Asp Trp Ser Ser Pro Gln
197 260 265 270
200 Val Phe Thr Thr Gln Asp Val Val Tyr Phe Pro Pro Lys Ile Leu Thr
201 275 280 285
204 Ser Val Gly Ser Asn Ala Ser Phe His Cys Ile Tyr Lys Asn Glu Asn
205 290 295 300
208 Gln Ile Ile Ser Ser Lys Gln Ile Val Trp Trp Arg Asn Leu Ala Glu
209 305 310 315 320
212 Lys Ile Pro Glu Ile Gln Tyr Ser Ile Val Ser Asp Arg Val Ser Lys
213 325 330 335
216 Val Thr Phe Ser Asn Leu Lys Ala Thr Arg Pro Arg Gly Lys Phe Thr
217 340 345 350
220 Tyr Asp Ala Val Tyr Cys Cys Asn Glu Gln Ala Cys His His Arg Tyr
221 355 360 365
224 Ala Glu Leu Tyr Val Ile Asp Val Asn Ile Asn Ile Ser Cys Glu Thr
225 370 375 380
228 Asp Gly Tyr Leu Thr Lys Met Thr Cys Arg Trp Ser Pro Ser Thr Ile
229 385 390 395 400
232 Gln Ser Leu Val Gly Ser Thr Val Gln Leu Arg Tyr His Arg Arg Ser
233 405 410 415
236 Leu Tyr Cys Pro Asp Ser Pro Ser Ile His Pro Thr Ser Glu Pro Lys
237 420 425 430
240 Asn Cys Val Leu Gln Arg Asp Gly Phe Tyr Glu Cys Val Phe Gln Pro
241 435 440 445
244 Ile Phe Leu Leu Ser Gly Tyr Thr Met Trp Ile Arg Ile Asn His Ser
245 450 455 460
248 Leu Gly Ser Leu Asp Ser Pro Pro Thr Cys Val Leu Pro Asp Ser Val
249 465 470 475 480
252 Val Lys Pro Leu Pro Pro Ser Asn Val Lys Ala Glu Ile Thr Val Asn
253 485 490 495
256 Thr Gly Leu Leu Lys Val Ser Trp Glu Lys Pro Val Phe Pro Glu Asn
257 500 505 510
260 Asn Leu Gln Phe Gln Ile Arg Tyr Gly Leu Ser Gly Lys Glu Ile Gln
261 515 520 525
264 Trp Lys Thr His Glu Val Phe Asp Ala Lys Ser Lys Ser Ala Ser Leu
265 530 535 540
268 Leu Val Ser Asp Leu Cys Ala Val Tyr Val Val Gln Val Arg Cys Arg

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269	545	550	555	560
272	Arg Leu Asp Gly Leu Gly Tyr Trp Ser Asn Trp Ser Ser Pro Ala Tyr			
273	565	570	575	
276	Thr Leu Val Met Asp Val Lys Val Pro Met Arg Gly Pro Glu Phe Trp			
277	580	585	590	
280	Arg Lys Met Asp Gly Asp Val Thr Lys Lys Glu Arg Asn Val Thr Leu			
281	595	600	605	
284	Leu Trp Lys Pro Leu Thr Lys Asn Asp Ser Leu Cys Ser Val Arg Arg			
285	610	615	620	
288	Tyr Val Val Lys His Arg Thr Ala His Asn Gly Thr Trp Ser Glu Asp			
289	625	630	635	640
292	Val Gly Asn Arg Thr Asn Leu Thr Phe Leu Trp Thr Glu Pro Ala His			
293	645	650	655	
296	Thr Val Thr Val Leu Ala Val Asn Ser Leu Gly Ala Ser Leu Val Asn			
297	660	665	670	
300	Phe Asn Leu Thr Phe Ser Trp Pro Met Ser Lys Val Ser Ala Val Glu			
301	675	680	685	
304	Ser Leu Ser Ala Tyr Pro Leu Ser Ser Ser Cys Val Ile Leu Ser Trp			
305	690	695	700	
308	Thr Leu Ser Pro Asp Asp Tyr Ser Leu Leu Tyr Leu Val Ile Glu Trp			
309	705	710	715	720
312	Lys Ile Leu Asn Glu Asp Asp Gly Met Lys Trp Leu Arg Ile Pro Ser			
313	725	730	735	
316	Asn Val Lys Lys Phe Tyr Ile His Asp Asn Phe Ile Pro Ile Glu Lys			
317	740	745	750	
320	Tyr Gln Phe Ser Leu Tyr Pro Val Phe Met Glu Gly Val Gly Lys Pro			
321	755	760	765	
324	Lys Ile Ile Asn Gly Phe Thr Lys Asp Ala Ile Asp Lys Gln Gln Asn			
325	770	775	780	
328	Asp Ala Gly Leu Tyr Val Ile Val Pro Ile Ile Ile Ser Ser Cys Val			
329	785	790	795	800
332	Leu Leu Leu Gly Thr Leu Leu Ile Ser His Gln Arg Met Lys Lys Leu			
333	805	810	815	
336	Phe Trp Asp Asp Val Pro Asn Pro Lys Asn Cys Ser Trp Ala Gln Gly			
337	820	825	830	
340	Leu Asn Phe Gln Lys Arg Thr Asp Thr Leu			
341	835	840		
344	<210> SEQ ID NO: 3			
345	<211> LENGTH: 2848			
346	<212> TYPE: DNA			
347	<213> ORGANISM: Mus musculus			
349	<220> FEATURE:			
350	<221> NAME/KEY: misc_feature	/		
351	<222> LOCATION: (44)..(44)			
352	<223> OTHER INFORMATION: N can be A, C, T or G			
355	<220> FEATURE:			
356	<221> NAME/KEY: misc_feature			
357	<222> LOCATION: (67)..(67)	/		
358	<223> OTHER INFORMATION: N can be A, C, T or G			

RAW SEQUENCE LISTING
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361 <220> FEATURE:
362 <221> NAME/KEY: misc_feature
363 <222> LOCATION: (234)..(234)
364 <223> OTHER INFORMATION: N can be A, C, T or G
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368 <221> NAME/KEY: misc_feature
369 <222> LOCATION: (483)..(483)
370 <223> OTHER INFORMATION: N can be A, C, T or G
373 <220> FEATURE:
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375 <222> LOCATION: (527)..(527)
376 <223> OTHER INFORMATION: N can be A, C, T or G
379 <220> FEATURE:
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381 <222> LOCATION: (564)..(564)
382 <223> OTHER INFORMATION: N can be A, C, T or G
385 <220> FEATURE:
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388 <223> OTHER INFORMATION: N can be A, C, T or G
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393 <222> LOCATION: (1335)..(1335)
394 <223> OTHER INFORMATION: N can be A, C, T or G
397 <220> FEATURE:
398 <221> NAME/KEY: misc_feature
399 <222> LOCATION: (2038)..(2038)
400 <223> OTHER INFORMATION: N can be A, C, T or G
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406 <223> OTHER INFORMATION: N can be A, C, T or G
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411 <222> LOCATION: (2182)..(2182)
412 <223> OTHER INFORMATION: N can be A, C, T or G
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416 <221> NAME/KEY: misc_feature
417 <222> LOCATION: (2183)..(2183)
418 <223> OTHER INFORMATION: N can be A, C, T or G
421 <220> FEATURE:
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423 <222> LOCATION: (2219)..(2219)
424 <223> OTHER INFORMATION: N can be A, C, T or G
427 <220> FEATURE:
428 <221> NAME/KEY: misc_feature
429 <222> LOCATION: (2576)..(2576)
430 <223> OTHER INFORMATION: N can be A, C, T or G
433 <220> FEATURE:

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; Xaa Pos. 29
Seq#:3; N Pos. 44, 67, 234, 483, 527, 564, 1237, 1335, 2038, 2179, 2182, 2183, 2219
Seq#:3; N Pos. 2576, 2610
Seq#:4; Xaa Pos. 79
Seq#:5; N Pos. 160, 258
Seq#:6; Xaa Pos. 14, 19, 25, 58, 67, 68, 84, 86
Seq#:35; N Pos. 5
Seq#:39; N Pos. 55, 62, 72, 143
Seq#:40; N Pos. 83, 101, 181
Seq#:41; N Pos. 193
Seq#:86; Xaa Pos. 29
Seq#:87; Xaa Pos. 29
Seq#:88; Xaa Pos. 29
Seq#:89; Xaa Pos. 79
Seq#:90; Xaa Pos. 14, 19, 25, 58, 67, 68, 84, 86
Seq#:91; Xaa Pos. 79
Seq#:92; Xaa Pos. 14, 19, 25, 58, 67, 68, 84, 86